

1/21

## SEQUENCE LISTING

RECEIVED

NOV 15 2000
TECH CENTER 1600/2900

60

403

85

<110> Segre, Gino V.
 Kronenberg, Henry M.
 Abou-Samra, Abdul-Badi
 Juppner, Harald
 Potts, Jr., John T.
 Schipani, Ernestina

## <120> PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME

<130> 00786/071005

<140> US 09/199,874

<141> 1998-11-24

<150> US 08/471,494

<151> 1995-06-06

<160> 28

<170> FastSEQ for Windows Version 4.0

75

90

<210> 1

<211> 1862

<212> DNA

<213> Didelphoidea

<220>

<221> CDS

<222> (98)...(1642)

<400> 1

gtggccccgt tggactcggc cctagggaac ggcggcg atg gga gcg ccc cgg atc Met Gly Ala Pro Arg Ile 1 5													
tcg cac agc ctt gcc ttg ctc ctc tgc tgc tcc gtg ctc ag Ser His Ser Leu Ala Leu Leu Leu Cys Cys Ser Val Leu Se 10 15													
tac gca ctg gtg gat gcc gat gat gtc ata acg aag gag ga Tyr Ala Leu Val Asp Ala Asp Asp Val Ile Thr Lys Glu Gl 25 30 35													
att ctt ctg cgc aat gcc cag gcc cag tgt gag cag cgc ct Ile Leu Leu Arg Asn Ala Gln Ala Gln Cys Glu Gln Arg Le 40 45 50													
gtc ctc agg gtc cct gaa ctt gct gaa tct gcc aaa gac tc Val Leu Arg Val Pro Glu Leu Ala Glu Ser Ala Lys Asp Tr 55 60 65													
agg tot goa aag aca aag aag gag aaa oot goa gaa aag ot Arg Ser Ala Lys Thr Lys Lys Glu Lys Pro Ala Glu Lys Le													

cag gca gag gag tcc agg gaa gtt tct gac agg agc cgg ctg cag gat Gln Ala Glu Glu Ser Arg Glu Val Ser Asp Arg Ser Arg Leu Gln Asp

95

tgggcacage caccetgttg gtagtecagg ggccageeca etgagetgge atateagetg

					gag Glu											451
gtg Val	ccc Pro 120	ggc Gly	aag Lys	gtg Val	gtg Val	gcc Ala 125	gtg Val	ccc Pro	tgc Cys	ccc Pro	gac Asp 130	tac Tyr	ttc Phe	tac Tyr	gac Asp	499
					cga Arg 140											547
					ggg Gly											595
					acc Thr											643
					tac Tyr											691
					ctg Leu											739
					cac His 220											787
					atc Ile											835
					cgc Arg											883
					gac Asp											931
gta Val	acc Thr 280	gtc Val	ttc Phe	ctt Leu	tac Tyr	ttc Phe 285	ctg Leu	acc Thr	acc Thr	aac Asn	tac Tyr 290	tac Tyr	tgg Trp	atc Ile	ctg Leu	979
gtg Val 295	gaa Glu	ggc Gly	ctc Leu	tac Tyr	ctt Leu 300	cac His	agc Ser	ctc Leu	atc Ile	ttc Phe 305	atg Met	gct Ala	ttt Phe	ttc Phe	tct Ser 310	1027
					tgg Trp											1075
gcc Ala	gtg Val	ttt Phe	gtc Val 330	gct Ala	gtg Val	tgg Trp	gtg Val	acc Thr 335	gtg Val	agg Arg	gct Ala	aca Thr	ctg Leu 340	gcc Ala	aac Asn	1123

act gag tgo Thr Glu Cys 345	Trp Asp	Leu Ser						1171
gtg ccc atc Val Pro Ile 360	ctg gca Leu Ala	gct att Ala Ile 365	gtg gtg Val Val	aac ttt Asn Phe	att ctt Ile Leu 370	ttt atc Phe Ile	aat Asn	1219
ata atc aga Ile Ile Arg 375								1267
tgt gac acg Cys Asp Thr								1315
ctc atg ccg Leu Met Pro								1363
tac aca gaa Tyr Thr Glu 425	Val Ser	Gly Ile						1411
atg ctc ttc Met Leu Phe 440	aat tca Asn Ser	ttc cag Phe Gln 445	gga ttt Gly Phe	ttc gtt Phe Val	gcc att Ala Ile 450	ata tac Ile Tyr		1459
ttc tgc aat Phe Cys Asn 455								1507
tgg acc ctg Trp Thr Leu							-	1555
acc tac ago Thr Tyr Ser	tat ggc Tyr Gly 490	ccc atg Pro Met	gtg tca Val Ser 495	cat aca His Thr	agt gtc Ser Val	acc aat Thr Asn 500	gtg Val	1603
gga cct cga Gly Pro Arg 505	Gly Gly	Trp.Pro				tageteet	egg	1652
ggctggagcc ttctgagaac caatggctct ggagagagag	tcattgcct ggactttat	t catctg g agccaa	gccc aga tggt tgg	agcctggc	accaaaga	atg acgg	gtatct ggagga	1712 1772 1832 1862
<210> 2 <211> 1863 <212> DNA <213> Didel	phoidea							

<220>

<221> CDS <222> (98)...(1852)

<400> 2 tgggcacage caccetgttg gtagtccagg ggccageeca etgagetgge atateagetg

gtggccccgt tggactcggc cctagggaac ggcggcg atg gga gcg ccc cgg atc Met Gly Ala Pro Arg Ile 1 5													
tcg cac agc ctt gcc ttg ctc ctc tgc tgc tcc gtg ctc agc tcc gtc Ser His Ser Leu Ala Leu Leu Cys Cys Ser Val Leu Ser Ser Val 10 15 20	163												
tac gca ctg gtg gat gcc gat gat gtc ata acg aag gag gag cag atc Tyr Ala Leu Val Asp Ala Asp Asp Val Ile Thr Lys Glu Glu Gln Ile 25 30 35	211												
att ctt ctg cgc aat gcc cag gcc cag tgt gag cag cgc ctg aaa gag Ile Leu Leu Arg Asn Ala Gln Ala Gln Cys Glu Gln Arg Leu Lys Glu 40 45 50	259												
gtc ctc agg gtc cct gaa ctt gct gaa tct gcc aaa gac tgg atg tca Val Leu Arg Val Pro Glu Leu Ala Glu Ser Ala Lys Asp Trp Met Ser 55 60 65 70	307												
agg tot goa aag aca aag gag aaa cot goa gaa aag ott tat coo Arg Ser Ala Lys Thr Lys Lys Glu Lys Pro Ala Glu Lys Leu Tyr Pro 75 80 85	355												
cag gca gag gag tcc agg gaa gtt tct gac agg agc cgg ctg cag gat Gln Ala Glu Glu Ser Arg Glu Val Ser Asp Arg Ser Arg Leu Gln Asp 90 95 100	403												
ggc ttc tgc cta cct gag tgg gac aac att gtg tgc tgg cct gct gga Gly Phe Cys Leu Pro Glu Trp Asp Asn Ile Val Cys Trp Pro Ala Gly 105 110 115	451												
gtg ccc ggc aag gtg gtg gcc gtg ccc tgc ccc gac tac ttc tac gac Val Pro Gly Lys Val Val Ala Val Pro Cys Pro Asp Tyr Phe Tyr Asp 120 125 130	499												
ttc aac cac aaa ggc cga gcc tat cgg cgc tgt gac agc aat ggc agc Phe Asn His Lys Gly Arg Ala Tyr Arg Arg Cys Asp Ser Asn Gly Ser 135 140 145 150	547												
tgg gag ctg gtg cct ggg aac aac cgg aca tgg gcg aat tac agc gaa Trp Glu Leu Val Pro Gly Asn Asn Arg Thr Trp Ala Asn Tyr Ser Glu 155 160 165	595												
tgt gtc aag ttt ctg acc aac gag acc cgg gaa cgg gaa gtc ttt gat Cys Val Lys Phe Leu Thr Asn Glu Thr Arg Glu Arg Glu Val Phe Asp 170 175 180	643												
cgc ctc gga atg atc tac act gtg ggc tac tcc atc tct ctg ggc tcc Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr Ser Ile Ser Leu Gly Ser 185 190 195	691												
ctc act gtg gct gtg ctg att ctg ggt tac ttt agg agg tta cat tgc Leu Thr Val Ala Val Leu Ile Leu Gly Tyr Phe Arg Arg Leu His Cys 200 205 210	739												
acc cga aac tac att cac atg cat ctc ttc gtg tcc ttt atg ctc cgg Thr Arg Asn Tyr Ile His Met His Leu Phe Val Ser Phe Met Leu Arg 215 220 225 230	787												

								gct Ala								835
aca Thr	gat Asp	gaa Glu	atc Ile 250	gag Glu	cgc Arg	atc Ile	acc Thr	gag Glu 255	gag Glu	gag Glu	ctg Leu	agg Arg	gcc Ala 260	ttc Phe	aca Thr	883
								ggt Gly								931
								acc Thr								979
								ctc Leu								1027
								aca Thr								1075
								acc Thr 335								1123
								ggg Gly								1171
								gtg Val								1219
								ctc Leu								1267
								aag Lys								1315
								tac Tyr 415								1363
								tgg Trp								1411
								ttt Phe								1459
								gag Glu								1507

tgg acc ctg gcc ttg gac ttc aag cgg aag gcc cgg agt ggc agc agt Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser 475 480 485	1555
acc tac agc tat ggc ccc atg gtg tca cat aca agt gtc acc aat gtg Thr Tyr Ser Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val 490 495 500	1603
gga cct cga ggg ggg ctg gcc ttg tcc ctc agc cct cga cta gct cct Gly Pro Arg Gly Gly Leu Ala Leu Ser Leu Ser Pro Arg Leu Ala Pro 505 510 515	1651
ggg gct gga gcc agt gcc aat ggc cat cac cag ttg cct ggc tat gtg Gly Ala Gly Ala Ser Ala Asn Gly His His Gln Leu Pro Gly Tyr Val 520 525 530	1699
aag cat ggt tcc att tct gag aac tca ttg cct tca tct ggc cca gag Lys His Gly Ser Ile Ser Glu Asn Ser Leu Pro Ser Ser Gly Pro Glu 535 540 545 550	1747
cct ggc acc aaa gat gac ggg tat ctc aat ggc tct gga ctt tat gag Pro Gly Thr Lys Asp Asp Gly Tyr Leu Asn Gly Ser Gly Leu Tyr Glu 555 560 565	1795
cca atg gtt ggg gaa cag ccc cct cca ctc ctg gag gag gag aga gag Pro Met Val Gly Glu Gln Pro Pro Pro Leu Leu Glu Glu Glu Arg Glu 570 575 580	1843
aca gtc atg tgacccatat c Thr Val Met 585	1863
<210> 3 <211> 2051 <212> DNA <213> Rattus rattus	
<220> <221> CDS <222> (73)(1845)	
<400> 3 ggcgggggcc gcggcggcga gctcggaggc cggcggcggc tgccccgagg gacgcggccc taggcggtgg cg atg ggg gcc gcc cgg atc gca ccc agc ctg gcg ctc cta Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu  1 5 10	60 111
ctc tgc tgc cca gtg ctc agc tcc gca tat gcg ctg gtg gat gcg gac Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Ala Leu Val Asp Ala Asp 15 20 25	159
gat gtc ttt acc aaa gag gaa cag att ttc ctg ctg cac cgt gcc cag Asp Val Phe Thr Lys Glu Glu Gln Ile Phe Leu Leu His Arg Ala Gln 30 35 40 45	207
gcg caa tgt gac aag ctg ctc aag gaa gtt ctg cac aca gca gcc aac Ala Gln Cys Asp Lys Leu Leu Lys Glu Val Leu His Thr Ala Ala Asn 50 55 60	255

					aag Lys											30	/3
					gca Ala											35	,1
					acc Thr											39	9
					atc Ile 115											44	7
					tgt Cys											49	5
					cgc Arg											54	.3
	222				acg Thr		_			_		_		_		59	1
					cgg Arg											63	9
					tac Tyr 195											68	7
					tat Tyr											73	5
					ttc Phe											78	3
					gtg Val											83	1
gag Glu	cgc Arg 255	ctc Leu	aca Thr	gag Glu	gaa Glu	gag Glu 260	ttg Leu	cac His	atc Ile	atc Ile	gcg Ala 265	cag Gln	gtg Val	cca Pro	cct Pro	87	9
					gcc Ala 275											92	7
acc Thr	ttc Ph	ttc Phe	ctc Leu	tac Tyr 290	ttc Phe	ctg Leu	gct Ala	acc Thr	aac Asn 295	tac Tyr	tac Tyr	tgg Trp	att Ile	ctg Leu 300	gtg Val	97	5

												ttt Phe				1023
												ggt Gly 330				1071
gtc Val	ttc Phe 335	gtg Val	gct Ala	gtg Val	tgg Trp	gtc Val 340	ggt Gly	gtc Val	aga Arg	gca Ala	acc Thr 345	ttg Leu	gcc Ala	aac Asn	act Thr	1119
												atc Ile				1167
												ttt Phe				1215
atc Ile	cgg Arg	gtg Val	ctt Leu 385	gcc Ala	act Thr	aag Lys	ctt Leu	cgg Arg 390	gag Glu	acc Thr	aat Asn	gcg Ala	ggc Gly 395	cgg Arg	tgt Cys	1263
												acg Thr 410				1311
gtg Val	ccg Pro 415	ctc Leu	ttt Phe	ggt Gly	gtc Val	cac His 420	tac Tyr	acc Thr	gtc Val	ttc Phe	atg Met 425	gcc Ala	ttg Leu	ccg Pro	tac Tyr	1359
acc Thr 430	gag Glu	gtc Val	tca Ser	Gly	aca Thr 435	ttg Leu	tgg Trp	cag Gln	atc Ile	cag Gln 440	atg Met	cat His	tat Tyr	gag Glu	atg Met 445	1407
												ata Ile				1455
												tgg Trp				1503
aca Thr	ctg Leu	gcg Ala 480	ttg Leu	gac Asp	ttc Phe	aag Lys	cgc Arg 485	aaa Lys	gca Ala	cga Arg	agt Ser	ggg Gly 490	agt Ser	agc Ser	agc Ser	1551
tac Tyr	agc Ser 495	tat Tyr	ggc Gly	cca Pro	atg Met	gtg Val 500	tct Ser	cac His	acg Thr	agt Ser	gtg Val 505	acc Thr	aat Asn	gtg Val	ggc Gly	1599
												ctg Leu				1647
act Thr	acc Thr	aat Asn	ggc Gly	cac His 530	tcc Ser	cag Gln	ctg Leu	cct Pro	ggc Gly 535	cat His	gcc Ala	aag Lys	cca Pro	ggg Gly 540	gct Ala	1695

9/21 8

cca gcc act gag act gaa acc cta cca gtc act atg gcg gtt ccc aag Pro Ala Thr Glu Thr Glu Thr Leu Pro Val Thr Met Ala Val Pro Lys 545 550 555	1743
gac gat gga ttc ctt aac ggc tcc tgc tca ggc ctg gat gag gac Asp Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala 560 565 570	1791
tcc ggg tct gcg ccg cct cca ttg ttg cag gaa gga tgg gaa aca Ser Gly Ser Ala Arg Pro Pro Pro Leu Leu Gln Glu Gly Trp Glu Thr 575 580 585	1839
gtc atg tgactgggca ctagggggct agactgctgg cctgggcaca tggacagatg Val Met 590	1895
gaccaagaag ccagtgtttg gctggttgtc tattcgggat ctggaccagg aagataacaa aaggaaaatg gaagtggacg aagcagagaa gaaggaagag gttttgcagg aattaaatat gtttcctcag ttggatgatg aggacacaag gaaggc	1955 2015 2051
<210> 4 <211> 2010 <212> DNA <213> Homo sapiens	
<220> <221> CDS <222> (28)(1806)	
<400> 4	
gggatcccgc ggccctaggc ggtggcg atg ggg acc gcc cgg atc gca ccc ggc Met Gly Thr Ala Arg Ile Ala Pro Gly 1 5	54
Met Gly Thr Ala Arg Ile Ala Pro Gly	54 102
Met Gly Thr Ala Arg Ile Ala Pro Gly  1 5  ctg gcg ctc ctg ctc tgc ccc gtg ctc agc tcc gcg tac gcg ctg Leu Ala Leu Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Ala Leu	
tcg gcg ctc ctg ctc tgc tgc ccc gtg ctc agc tcc gcg tac gcg ctg Leu Ala Leu Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Ala Leu 10 15 20 25  gtg gat gca gat gac gtc atg act aaa gag gaa cag atc ttc ctg ctg Val Asp Ala Asp Asp Val Met Thr Lys Glu Glu Gln Ile Phe Leu Leu	102
tcg gcg ctc ctg ctc tgc tgc ccc gtg ctc agc tcc gcg tac gcg ctg Leu Ala Leu Leu Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Ala Leu 10 15 20 25  gtg gat gca gat gac gtc atg act aaa gag gaa cag atc ttc ctg ctg Val Asp Ala Asp Asp Val Met Thr Lys Glu Glu Gln Ile Phe Leu Leu 30 35 40  cac cgt gct cag gcc cag tgc gaa aaa cgg ctc aag gag gtc ctg cag His Arg Ala Gln Ala Gln Cys Glu Lys Arg Leu Lys Glu Val Leu Gln	102 150
ctg gcg ctc ctg ctc tgc tgc ccc gtg ctc agc tcc gcg tac gcg ctg Leu Ala Leu Leu Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Ala Leu 10 15 20 25  gtg gat gca gat gac gtc atg act aaa gag gaa cag atc ttc ctg ctg Val Asp Ala Asp Asp Val Met Thr Lys Glu Glu Gln Ile Phe Leu Leu 30 35 40  cac cgt gct cag gcc cag tgc gaa aaa cgg ctc aag gag gtc ctg cag His Arg Ala Gln Ala Gln Cys Glu Lys Arg Leu Lys Glu Val Leu Gln 45 50 55  agg cca gcc agc ata atg gaa tca gac aag gga tgg aca tct gcg tcc Arg Pro Ala Ser Ile Met Glu Ser Asp Lys Gly Trp Thr Ser Ala Ser	102 150 198
ctg gcg ctc ctg ctc tgc tgc ccc gtg ctc agc tcc gcg tac gcg ctg Leu Ala Leu Leu Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Ala Leu 10 15 20 25  gtg gat gca gat gac gtc atg act aaa gag gaa cag atc ttc ctg ctg Val Asp Ala Asp Asp Val Met Thr Lys Glu Glu Gln Ile Phe Leu Leu 30 35 40  cac cgt gct cag gcc cag tgc gaa aaa cgg ctc aag gag gtc ctg cag His Arg Ala Gln Ala Gln Cys Glu Lys Arg Leu Lys Glu Val Leu Gln 45 50 55  agg cca gcc agc ata atg gaa tca gac aag gga tgg aca tct gcg tcc Arg Pro Ala Ser Ile Met Glu Ser Asp Lys Gly Trp Thr Ser Ala Ser 60 65 70  aca tca ggg aag ccc agg aaa gat aag gca tct ggg aag ctc tac cct Thr Ser Gly Lys Pro Arg Lys Asp Lys Ala Ser Gly Lys Leu Tyr Pro	102 150 198 246

gca Ala	cca Pro	ggt Gly	gag Glu 125	gtg Val	gtg Val	gct Ala	gtg Val	ccc Pro 130	tgt Cys	ccg Pro	gac Asp	tac Tyr	att Ile 135	tat Tyr	gac Asp	438
											gac Asp					486
											gcc Ala 165					534
											cgg Arg					582
											gtg Val					630
											agg Arg					678
											tcc Ser					726
											tac Tyr 245					774
ctt Leu 250	gat Asp	gag Glu	gct Ala	gag Glu	cgc Arg 255	ctc Leu	acc Thr	gag Glu	gag Glu	gag Glu 260	ctg Leu	cgc Arg	gcc Ala	atc Ile	gcc Ala 265	822
											ggc Gly					870
											gcc Ala					918
tgg Trp	att Ile	ctg Leu 300	gtg Val	gag Glu	ggg ggg	ctg Leu	tac Tyr 305	ctg Leu	cac His	agc Ser	ctc Leu	atc Ile 310	ttc Phe	atg Met	gcc Ala	966
											aca Thr 325					1014
ggt Gly 330	ctg Leu	ccc Pro	gct Ala	gtc Val	ttc Phe 335	gtg Val	gct Ala	gtg Val	tgg Trp	gtc Val 340	agt Ser	gtc Val	aga Arg	gct Ala	acc Thr 345	1062
											ggg Gly					1110

atc Ile	atc Ile	cag Gln	gtg Val 365	ccc Pro	atc Ile	ctg Leu	gcc Ala	tcc Ser 370	att Ile	gtg Val	ctc Leu	aac Asn	ttc Phe 375	atc Il	ctc Leu	1158
		aat Asn 380														1206
		cgg Arg														1254
		gtg Val														1302
		cca Pro														1350
		gag Glu														1398
ata Ile	tac Tyr	tgt Cys 460	ttc Phe	tgc Cys	aat Asn	ggc Gly	gag Glu 465	gta Val	caa Gln	gct Ala	gag Glu	atc Ile 470	aag Lys	aaa Lys	tct Ser	1446
		cgc Arg														1494
		agc Ser														1542
acc Thr	aat Asn	gtc Val	ggc Gly	ccc Pro 510	cgt Arg	gtg Val	gga Gly	ctc Leu	ggc Gly 515	ctg Leu	ccc Pro	ctc Leu	agc Ser	ccc Pro 520	cgc Arg	1590
		ccc Pro														1638
		cca Pro 540														1686
gcc Ala	atg Met 555	gct Ala	gct Ala	ccc Pro	aag Lys	gac Asp 560	gat Asp	G1A G3G	ttc Phe	ctc Leu	aac Asn 565	ggc Gly	tcc Ser	tgc Cys	tca Ser	1734
ggc Gly 570	ctg Leu	gac Asp	gag Glu	gag Glu	gcc Ala 575	tct Ser	ggg Gly	cct Pro	gag Glu	cgg Arg 580	cca Pro	cct Pro	gcc Ala	ctg Leu	cta Leu 585	1782
		gag Glu						tgad	cago	gcg (	etggg	gggct	g ga	accto	gctga	1836
cata tggg	gtgc	gat q aag a	ggaca aggaa	agato aaaa	gg ac	ccaa gggga	aagat aaaa	ggg a aga	gtggt aaaa	tga aaaa	atga aaga	attto aaaa	ccc a	actca gaaaa	agggcc aaaaaa	1896 1956

```
<210> 9
<211> 18
<212> PRT
<213> Artificial Sequence
<223> binding; 1st to last; peptide fragment
<400> 9
Pro Tyr Thr Glu Tyr Ser Gly Thr Leu Trp Gln Ile Gln Met His Tyr
Glu Met
<210> 10
<211> 18
<212> PRT
<213> Artificial Sequence
<220>
<223> binding; 1st to last; peptide fragment
Asp Asp Val Phe Thr Lys Glu Glu Gln Ile Phe Leu Leu His Arg Ala
Gln Ala
<210> 11
<211> 10
<212> PRT
<213> Artificial Sequence
<220>
<223> binding; 1st to last; peptide fragment
<400> 11
Phe Phe Arg Leu His Cys Thr Arg Asn Tyr
<210> 12
<211> 10
<212> PRT
<213> Artificial Sequence
<223> binding; 1st to last; peptide fragment
<400> 12
Glu Lys Lys Tyr Leu Trp Gly Phe Thr Leu
<210> 13
<211> 25
<212> PRT
<213> Artificial Sequence
<220>
<223> binding; 1st to last; peptide fragment
```

## 14/21

<400 Val 1		13 u Ala	Thr	Lys 5	Leu	Arg	Glu	Thr	Asn 10	Ala	Gly	Arg	Сув	Asp 15	Thr		
	Gl	n Gln	Tyr 20	_	Lys	Leu	Leu	Lys 25	10					10			
<210 <211 <212 <213	L> 2>	18	icia	l Sed	quen	ce											
<220 <223		lst t	o la	st; ]	prime	er											
<400 agat		14 ggct	gtgc	aggt												1	.8
<210 <211 <212 <213	L> ?> :	25	icia	l Sed	quenc	ce											
<220 <223		lst t	o la	st; ]	prime	er											
<400 ggaa		15 ccat	ggga	gegge	ee eq	ggat										2	5
<210 <211 <212 <213	L> : 2> :	24	icia	l Sed	quen	ce											
<220 <223		lst t	o la	st; ]	prime	er											
<400 cggg		16 cccg	cggc	cctaq	gg c	ggt										2	4
<210 <211 <212 <213	L> ≥> :	19	icia	l Sed	quenc	ce											
<220 <223		lst t	o la:	st; ]	prime	er											
<400 agta		17 gcgt	cctt	gacga	a											1	.9
<210 <211 <212 <213	>    >	515	phoi	dea													
_		18 y Ala	Pro	_	Ile	Ser	His	Ser		Ala	Leu	Leu	Leu	Cys 15	Сув		
1 Ser	۷a	l Leu	Ser 20	5 Ser	Val	Tyr	Ala	Leu 25	10 Val	Asp	Ala	Asp	Asp 30		Ile		
Thr	Ly	s Glu	Glu	Gln	Ile	Ile	Leu 40		Arg	Asn	Ala	Gln 45		Gln	Cys		

Glu Gln Arg Leu Lys Glu Val Leu Arg Val Pro Glu L u Ala Glu Ser Ala Lys Asp Trp Met Ser Arg Ser Ala Lys Thr Lys Lys Glu Lys Pro Ala Glu Lys Leu Tyr Pro Gln Ala Glu Glu Ser Arg Glu Val Ser Asp Arg Ser Arg Leu Gln Asp Gly Phe Cys Leu Pro Glu Trp Asp Asn Ile Val Cys Trp Pro Ala Gly Val Pro Gly Lys Val Val Ala Val Pro Cys Pro Asp Tyr Phe Tyr Asp Phe Asn His Lys Gly Arg Ala Tyr Arg Arg Cys Asp Ser Asn Gly Ser Trp Glu Leu Val Pro Gly Asn Asn Arg Thr Trp Ala Asn Tyr Ser Glu Cys Val Lys Phe Leu Thr Asn Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr Ser Ile Ser Leu Gly Ser Leu Thr Val Ala Val Leu Ile Leu Gly Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Leu Phe Val Ser Phe Met Leu Arg Ala Val Ser Ile Phe Ile Lys Asp Ala Val Leu Tyr Ser Gly Val Ser Thr Asp Glu Ile Glu Arg Ile Thr Glu Glu Glu Leu Arg Ala Phe Thr Glu Pro Pro Pro Ala Asp Lys Ala Gly Phe Val Gly Cys Arg Val Ala Val Thr Val Phe Leu Tyr Phe Leu Thr Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly Phe Thr Leu Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp Val Thr Val Arg Ala Thr Leu Ala Asn Thr Glu Cys Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ala Ile Val Val Asn Phe Ile Leu Phe Ile Asn Ile Ile Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu Val Ser Gly Ile Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Thr Tyr Ser Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Gly Gly Trp Pro Cys Pro Ser Ala Leu Asp

<210> 19 <211> 585 <212> PRT <213> Didelphoid a

<400> 19 Met Gly Ala Pro Arg Ile Ser His Ser Leu Ala Leu Leu Cys Cys Ser Val Leu Ser Ser Val Tyr Ala Leu Val Asp Ala Asp Asp Val Ile Thr Lys Glu Glu Gln Ile Ile Leu Leu Arg Asn Ala Gln Ala Gln Cys Glu Gln Arg Leu Lys Glu Val Leu Arg Val Pro Glu Leu Ala Glu Ser Ala Lys Asp Trp Met Ser Arg Ser Ala Lys Thr Lys Lys Glu Lys Pro Ala Glu Lys Leu Tyr Pro Gln Ala Glu Glu Ser Arg Glu Val Ser Asp Arg Ser Arg Leu Gln Asp Gly Phe Cys Leu Pro Glu Trp Asp Asn Ile Val Cys Trp Pro Ala Gly Val Pro Gly Lys Val Val Ala Val Pro Cys Pro Asp Tyr Phe Tyr Asp Phe Asn His Lys Gly Arg Ala Tyr Arg Arg Cys Asp Ser Asn Gly Ser Trp Glu Leu Val Pro Gly Asn Asn Arg Thr Trp Ala Asn Tyr Ser Glu Cys Val Lys Phe Leu Thr Asn Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr Ser Ile Ser Leu Gly Ser Leu Thr Val Ala Val Leu Ile Leu Gly Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Leu Phe Val Ser Phe Met Leu Arg Ala Val Ser Ile Phe Ile Lys Asp Ala Val Leu Tyr Ser Gly Val Ser Thr Asp Glu Ile Glu Arg Ile Thr Glu Glu Glu Leu Arg Ala Phe Thr Glu Pro Pro Pro Ala Asp Lys Ala Gly Phe Val Gly Cys Arg Val Ala Val Thr Val Phe Leu Tyr Phe Leu Thr Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly Phe Thr Leu Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp Val Thr Val Arg Ala Thr Leu Ala Asn Thr Glu Cys Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ala Ile Val Val Asn Phe Ile Leu Phe Ile Asn Ile Ile Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu Val Ser Gly Ile Leu Trp Gln 

Val Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln Gly Phe Phe 435 440 445 Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Thr Tyr Ser Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Gly Gly Leu Ala Leu Ser Leu Ser Pro Arg Leu Ala Pro Gly Ala Gly Ala Ser Ala Asn Gly His His Gln Leu Pro Gly Tyr Val Lys His Gly Ser Ile Ser Glu Asn Ser Leu Pro Ser Ser Gly Pro Glu Pro Gly Thr Lys Asp Asp Gly Tyr Leu Asn Gly Ser Gly Leu Tyr Glu Pro Met Val Gly Glu Gln Pro Pro Leu Leu Glu Glu Glu Arg Glu Thr Val Met 

<210> 20 <211> 591 <212> PRT

<213> Rattus rattus

<400> 20 Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Ala Leu Val Asp Ala Asp Asp Val Phe Thr Lys Glu Glu Gln Ile Phe Leu Leu His Arg Ala Gln Ala Gln Cys Asp Lys Leu Leu Lys Glu Val Leu His Thr Ala Ala Asn Ile Met Glu Ser Asp Lys Gly Trp Thr Pro Ala Ser Thr Ser Gly Lys Pro Arg Lys Glu Lys Ala Ser Gly Lys Phe Tyr Pro Glu Ser Lys Glu Asn Lys Asp Val Pro Thr Gly Ser Arg Arg Arg Gly Arg Pro Cys Leu Pro Glu Trp Asp Asn Ile Val Cys Trp Pro Leu Gly Ala Pro Gly Glu Val Val Ala Val Pro Cys Pro Asp Tyr Ile Tyr Asp Phe Asn His Lys Gly His Ala Tyr Arg Arg Cys Asp Arg Asn Gly Ser Trp Glu Val Val Pro Gly His Asn Arg Thr Trp Ala Asn Tyr Ser Glu Cys Leu Lys Phe Met Thr Asn Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr Ser Met Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Met Phe Leu Ser Phe Met Leu Arg Ala Ala Ser Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly Phe Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu Glu Leu His Ile Ile Ala Gln Val Pro Pro Pro Ala Ala Ala Val Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe 

```
Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu
                        295
                                            300
Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr
                    310
                                        315
Leu Trp Gly Phe Thr Ile Phe Gly Trp Gly Leu Pro Ala Val Phe Val
               325
                                   330
                                                        335
Ala Val Trp Val Gly Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp
                               345
Asp Leu Ser Ser Gly His Lys Lys Trp Ile Ile Gln Val Pro Ile Leu
        355
                            360
                                                365
Ala Ser Val Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Ile Arg Val
                        375
                                            380
Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg
                    39Õ
                                        395
Gln Gln Tyr Arg Lys Leu Leu Arg Ser Thr Leu Val Leu Val Pro Leu
                405
                                    410
Phe Gly Val His Tyr Thr Val Phe Met Ala Leu Pro Tyr Thr Glu Val
            420
                               425
                                                   430
Ser Gly Thr Leu Trp Gln Ile Gln Met His Tyr Glu Met Leu Phe Asn
        435
                            440
                                                445
Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly
   450
                       455
                                           460
Glu Val Gln Ala Glu Ile Arg Lys Ser Trp Ser Arg Trp Thr Leu Ala
                   470
                                       475
Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
                                   490
               485
Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Ala
                                505
Gly Leu Ser Leu Pro Leu Ser Pro Arg Leu Pro Pro Ala Thr Thr Asn
        515
                            520
                                                525
Gly His Ser Gln Leu Pro Gly His Ala Lys Pro Gly Ala Pro Ala Thr
                        535
                                            540
Glu Thr Glu Thr Leu Pro Val Thr Met Ala Val Pro Lys Asp Asp Gly
                    550
                                        555
Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly Ser
                565
                                    570
Ala Arg Pro Pro Pro Leu Leu Gln Glu Gly Trp Glu Thr Val Met
            580
                                585
```

<210> 21 <211> 593

<212> PRT <213> Homo sapiens

<400> 21

Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Ala Leu Val Asp Ala Asp Asp Val Met Thr Lys Glu Glu Gln Ile Phe Leu Leu His Arg Ala Gln Ala Gln Cys Glu Lys Arg Leu Lys Glu Val Leu Gln Arg Pro Ala Ser Ile Met Glu Ser Asp Lys Gly Trp Thr Ser Ala Ser Thr Ser Gly Lys Pro Arg Lys Asp Lys Ala Ser Gly Lys Leu Tyr Pro Glu Ser Glu Glu Asp Lys Glu Ala Pro Thr Gly Ser Arg Tyr Arg Gly Arg Pro Cys Leu Pro Glu Trp Asp His Ile Leu Cys Trp Pro Leu Gly Ala Pro Gly Glu Val Val Ala 

Val	Pro	Сув	Pro	Asp	Tyr	Ile	Tyr	Asp	Phe	Asn	His	Lys	Gly	His	Ala
Tyr	130 Arg	Arq	Cys	Asp	Arg	135 Asn	Gly	Ser	Trp	Glu	140 Leu	Val	Pro	Gly	His
145					150					155					160
Asn	Arg	Thr	Trp	Ala 165	Asn	Tyr	Ser	Glu	Сув 170	Val	Lys	Phe	Leu	Thr 175	Asn
Glu	Thr	Arg	Glu 180	Arg	Glu	Val	Phe	Asp 185	Arg	Leu	Gly	Met	Ile 190	Tyr	Thr
Val	Gly	Tyr 195	Ser	Val	Ser	Leu	Ala 200	Ser	Leu	Thr	Val	Ala 205	Val	Leu	Ile
Leu	Ala 210	Tyr	Phe	Arg	Arg	Leu 215	His	Сла	Thr	Arg	Asn 220	Tyr	Ile	His	Met
His 225	Leu	Phe	Leu	Ser	Phe 230	Met	Leu	Arg	Ala	Val 235	Ser	Ile	Phe	Val	Lys 240
Asp	Ala	Val	Leu	Tyr 245	Ser	Gly	Ala	Thr	Leu 250	Asp	Glu	Ala	Glu	Arg 255	Leu
Thr	Glu	Glu	Glu 260	Leu	Arg	Ala	Ile	Ala 265	Gln	Ala	Pro	Pro	Pro 270	Pro	Ala
Thr	Ala	Ala 275	Ala	Gly	Tyr	Ala	Gly 280	Сув	Arg	Val	Ala	Val 285	Thr	Phe	Phe
Leu	Tyr 290	Phe	Leu	Ala	Thr	Asn 295	Tyr	Tyr	Trp	Ile	Leu 300	Val	Glu	Gly	Leu
Tyr 305	Leu	His	Ser	Leu	Ile 310	Phe	Met	Ala	Phe	Phe 315	Ser	Glu	Lys	Lys	Tyr 320
Leu	Trp	Gly	Phe	Thr 325	Val	Phe	Gly	Trp	Gly 330	Leu	Pro	Ala	Val	Phe 335	Val
Ala	Val	Trp	Val 340	Ser	Val	Arg	Ala	Thr 345	Leu	Ala	Asn	Thr	Gly 350	Сув	Trp
Asp	Leu	Ser 355	Ser	Gly	Asn	Lys	360 Lys	Trp	Ile	Ile	Gln	<b>Val</b> 365	Pro	Ile	Leu
	Ser 370					375					380			_	
Leu 385	Ala	Thr	Lys	Gln	Arg 390	Glu	Thr	Asn	Ala	Gly 395	Arg	Cys	Asp	Thr	Arg 400
Gln	Gln	Tyr	Arg	Lys 405	Leu	Leu	Lys	Ser	Thr 410	Leu	Val	Leu	Met	Pro 415	Leu
	Gly		420	_				425				_	430		
	Gly	435					440			-		445			
	Phe 450		_			455				_	460		_		_
465	Val				470	_	_		_	475	_	_			480
	Asp			485					490					495	
_	Pro		500					505				-	510		
_	Leu	515					520	_				525			
	Gly 530					535	_				540				
545	Glu				550					555				_	560
	Gly			565					570					575	
Gly	Pro	Glu	Arg 580	Pro	Pro	Ala	Leu	Leu 585	Gln	Glu	Glu	Trp	Glu 590	Thr	Val
Met															

```
<210> 22
<211> 19
<212> PRT
<213> Rattus rattus
<400> 22
Val Gly Tyr Ser Met Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile
                  5
                                     10
Leu Ala Tyr
<210> 23
<211> 18
<212> PRT
<213> Rattus rattus
Ile His Met His Met Phe Leu Ser Phe Met Leu Arg Ala Ala Ser Phe
                                      10
 1
Val Lys
<210> 24
<211> 17
<212> PRT
<213> Rattus rattus
<400> 24
Leu Val Glu Gly Leu Tyr Leu Met Ser Leu Ile Phe Met Ala Phe Phe
                  5
                                      10
Ser
<210> 25
<211> 17
<212> PRT
<213> Rattus rattus
<400> 25
Val Gly Val Trp Val Ala Val Phe Val Ala Pro Leu Gly Trp Gly Phe
Ile
<210> 26
<211> 18
<212> PRT
<213> Rattus rattus
<400> 26
Arg His Asn Ile Phe Leu Ile Phe Asn Leu Val Val Ser Ala Leu Ile
                                      10
Pro Val
<210> 27
<211> 20
<212> PRT
<213> Rattus rattus
```

## 21/21

<210> 28 <211> 18 <212> PRT <213> Rattus rattus